

Localisation of exonic SNPs on one of the three alternative forms:

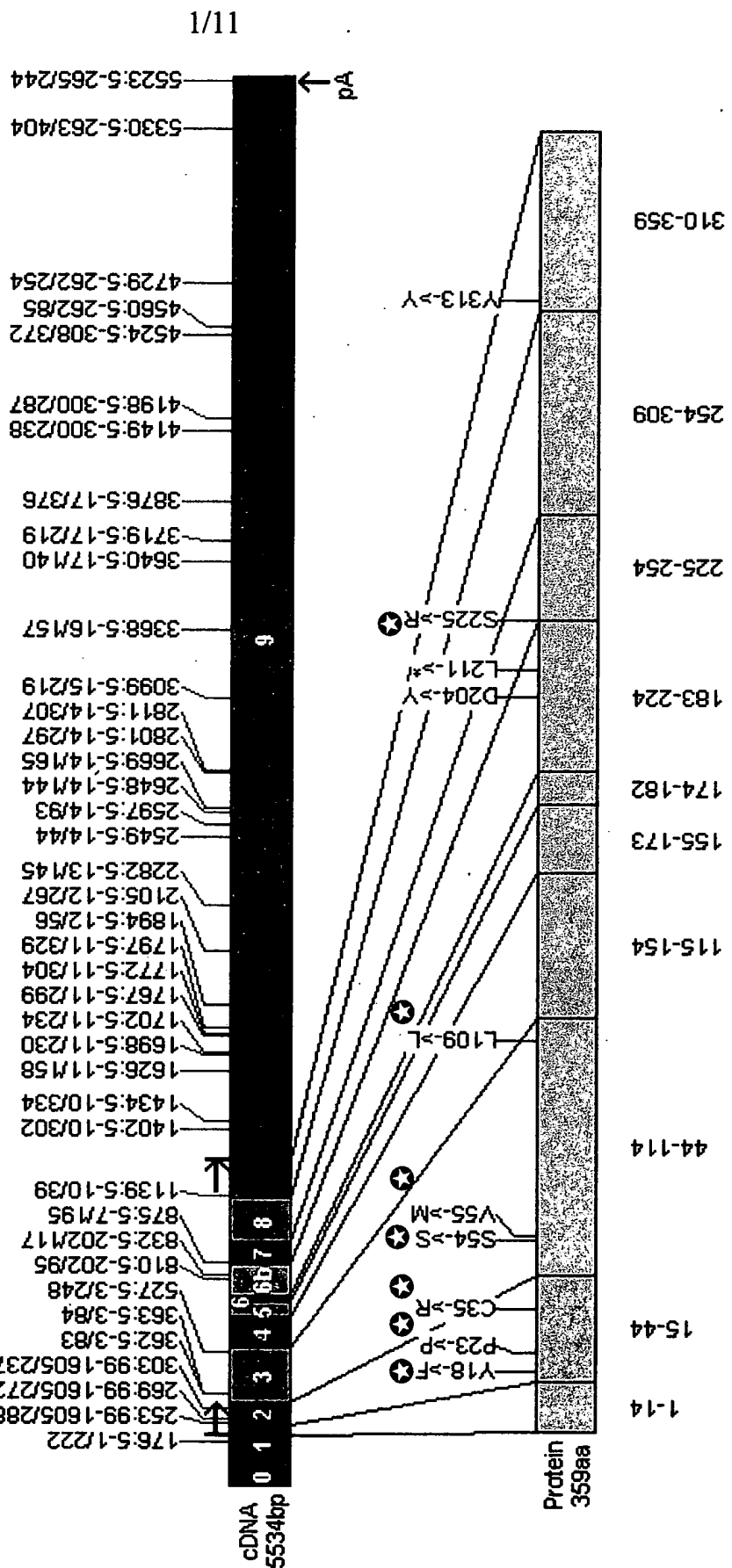


Figure 1A

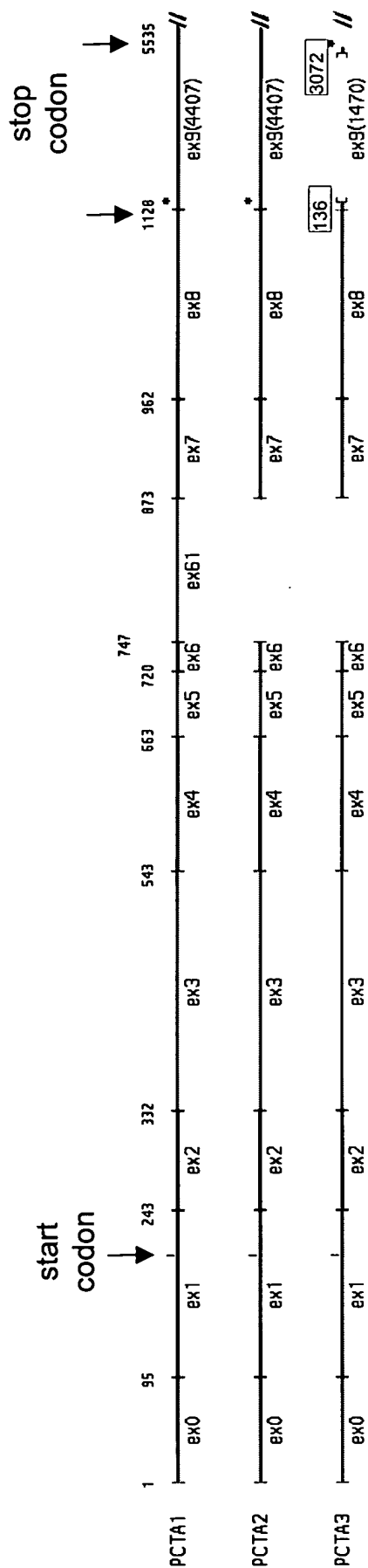


FIG. 1B

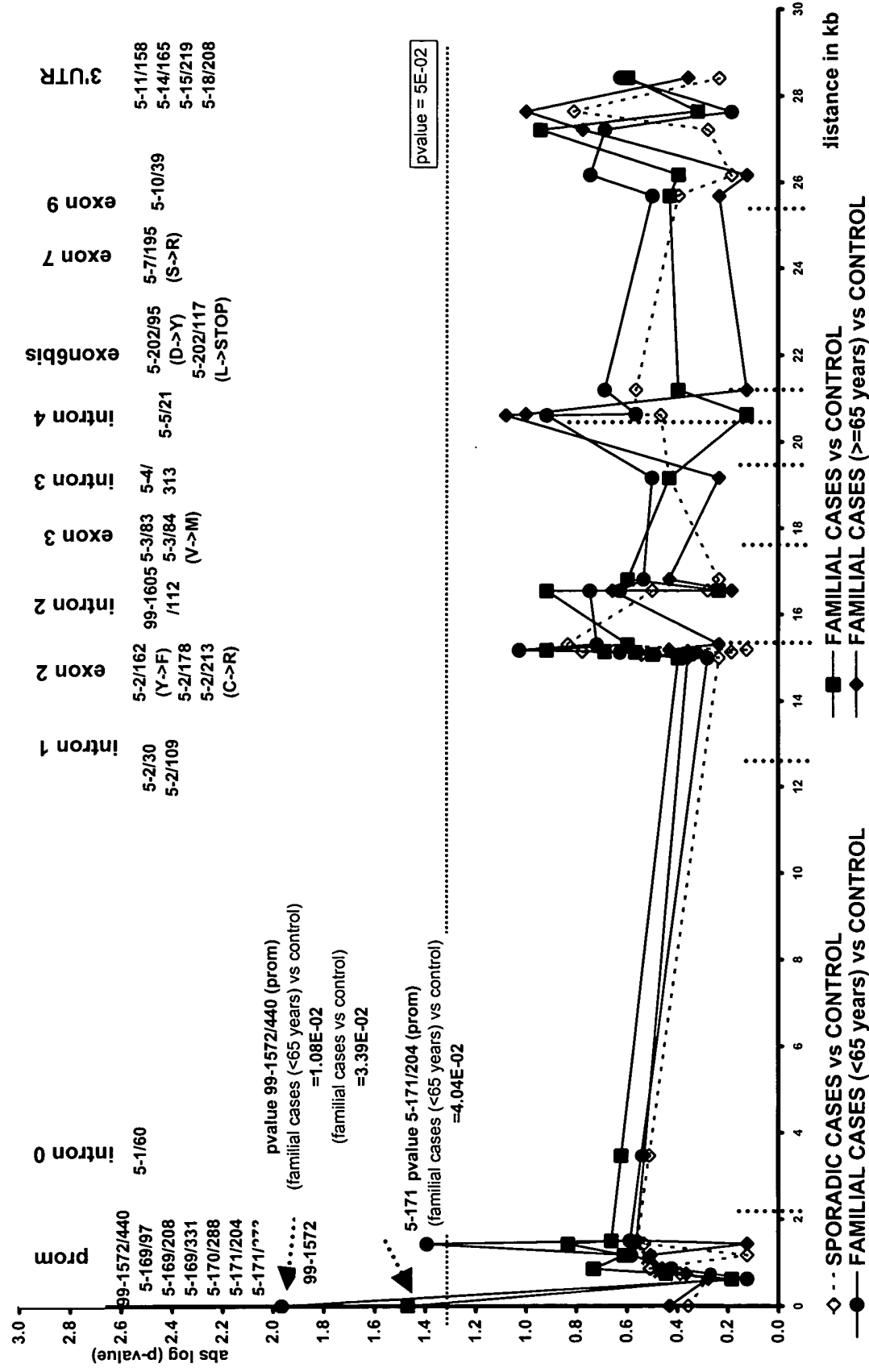


FIG. 2



4/11

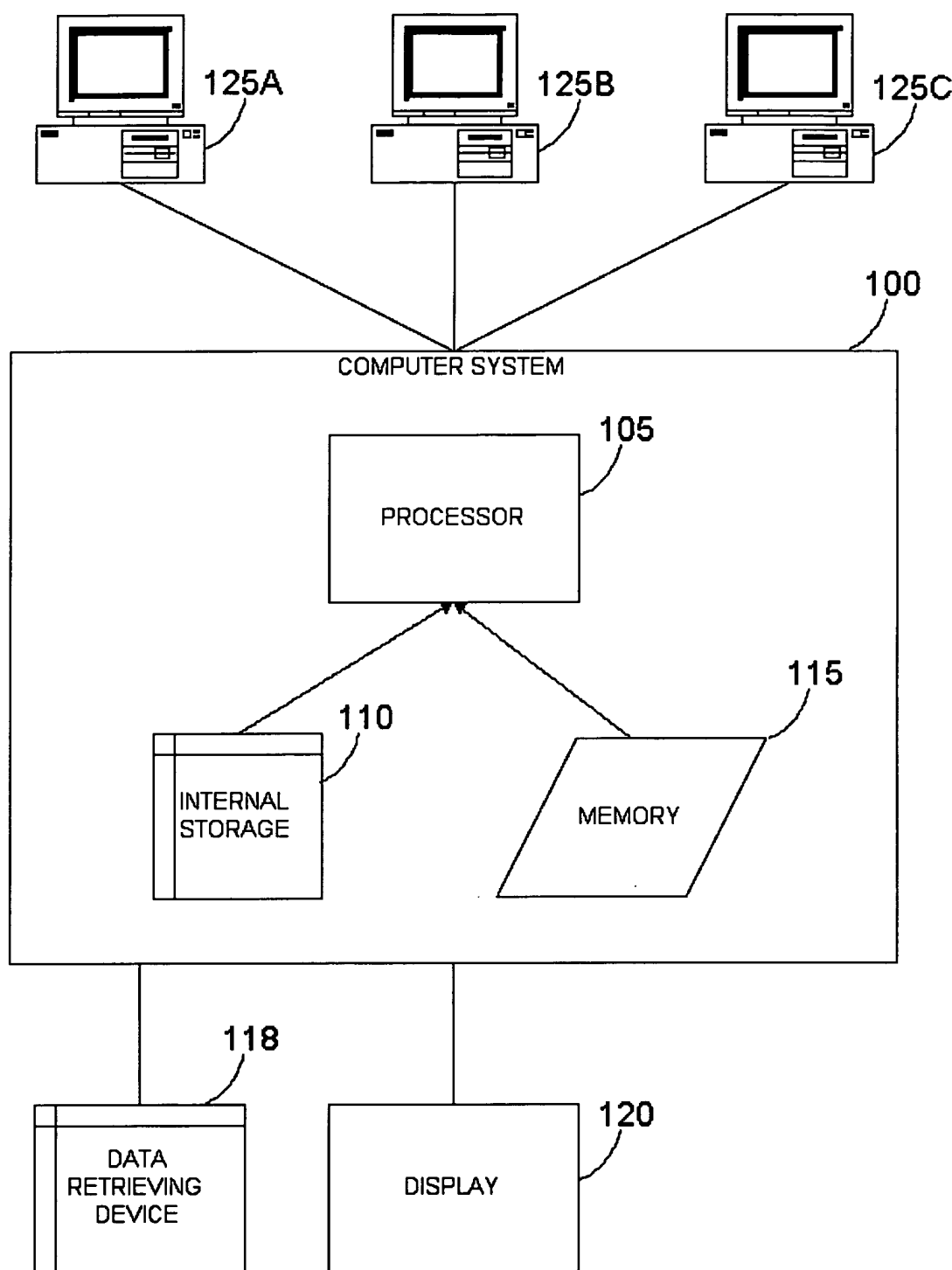


FIG. 3

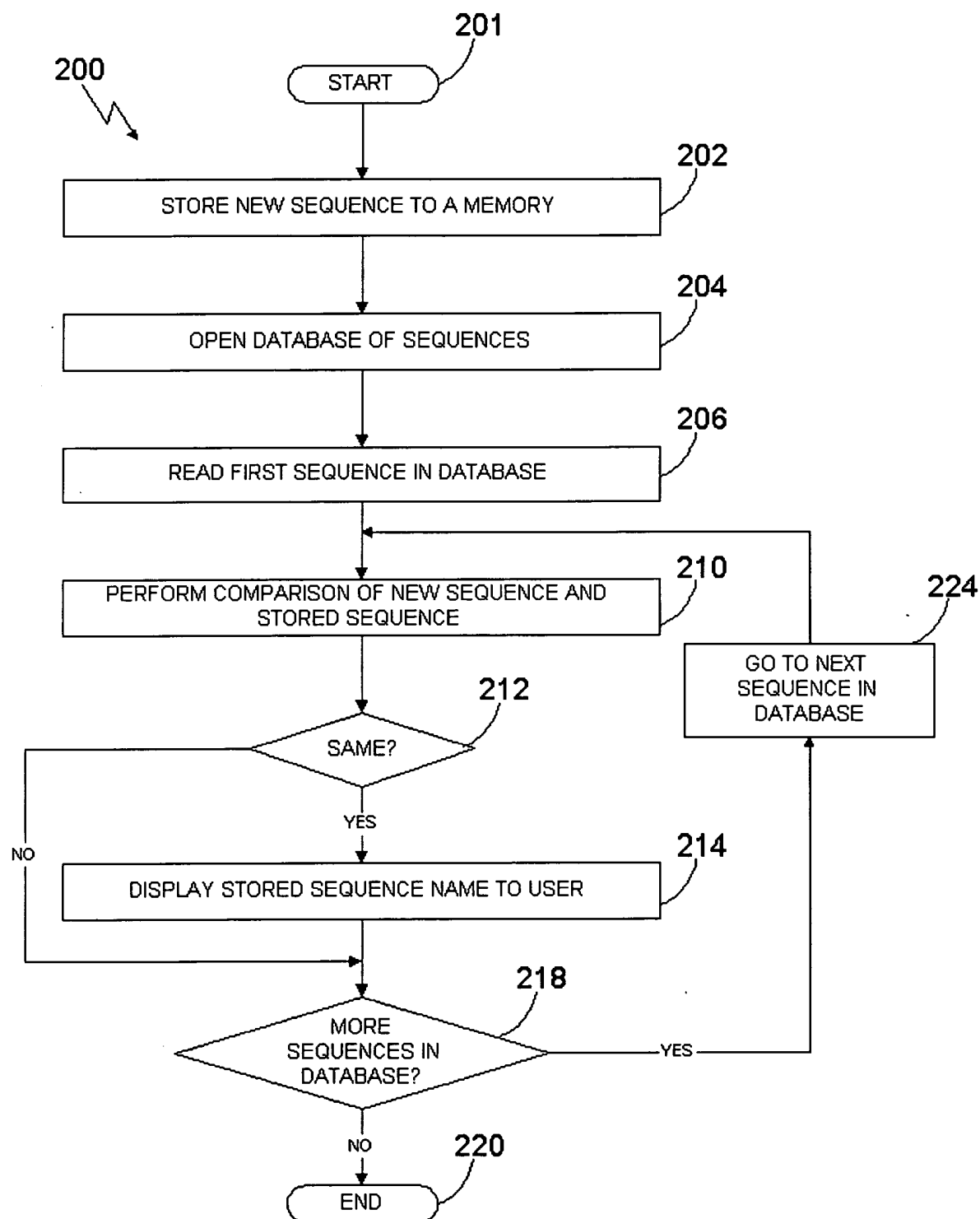


FIG. 4



6/11

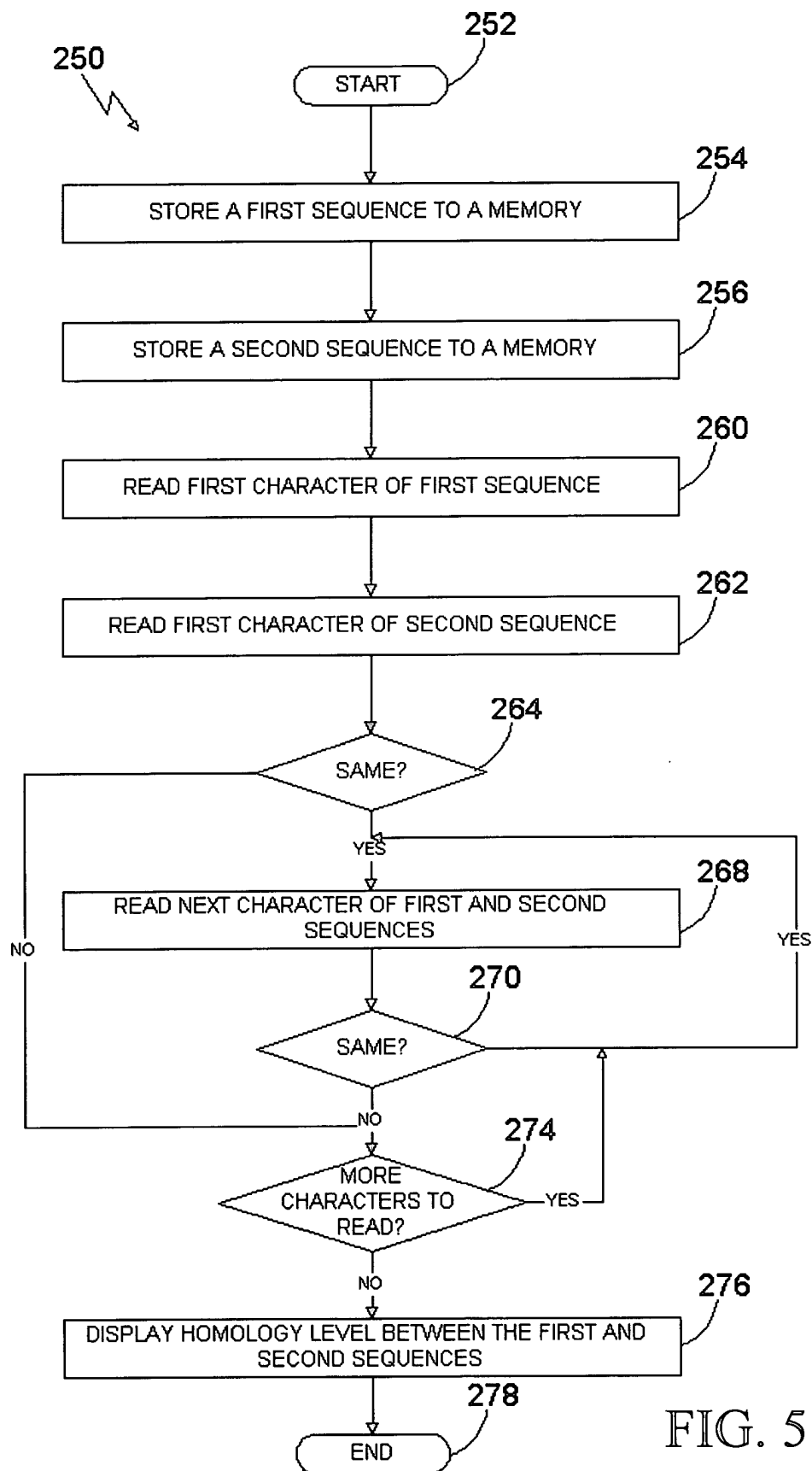


FIG. 5



7/11

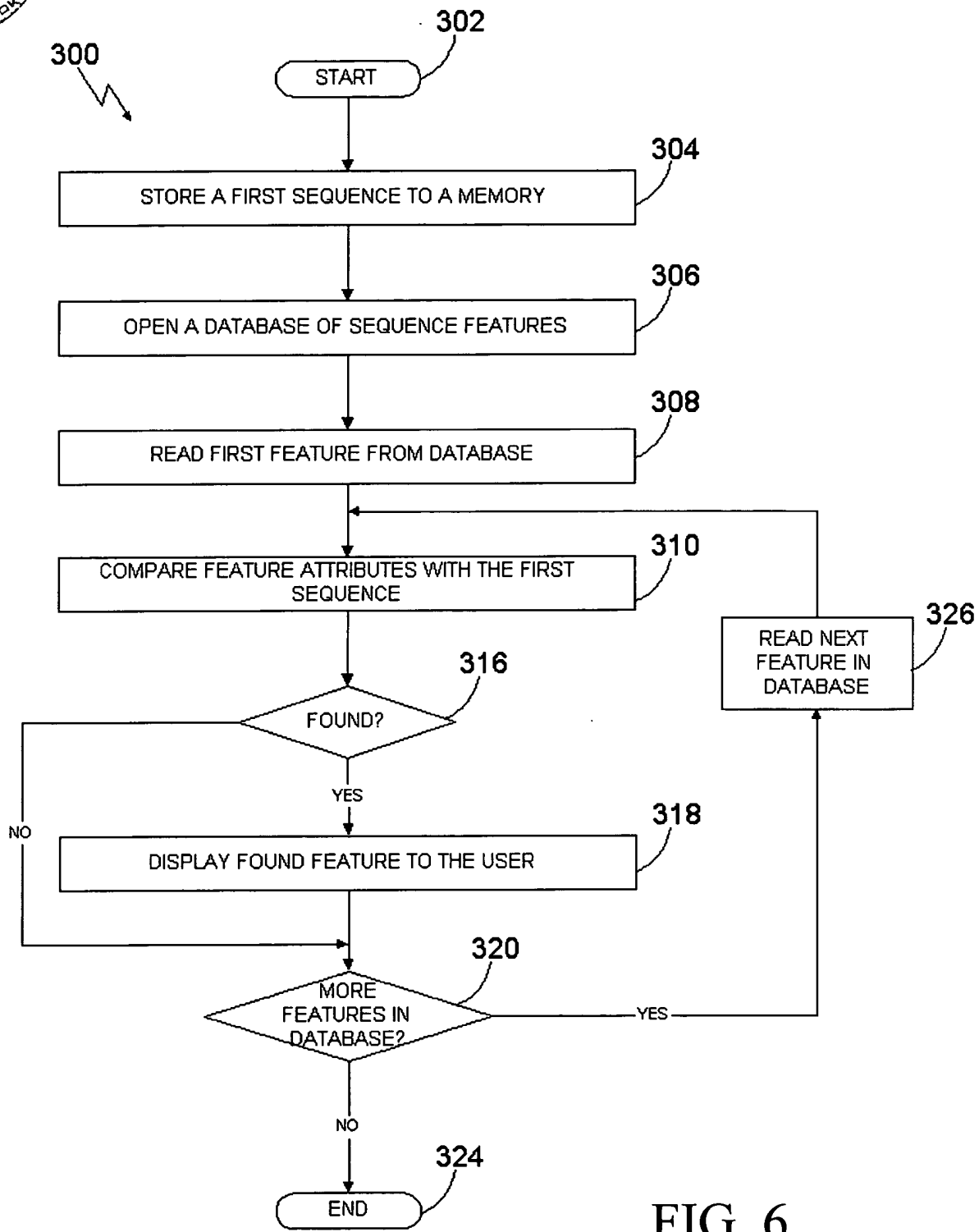


FIG. 6

8/11

	1					50
leg2	-----	-----	-----	-----	-----	-----
leg1	-----	-----	-----	-----	-----	-----
PCTA	-----	-----	-----	-----	-----	-----
PCTA.var	-----	-----	-----	-----	-----	-----
PCTA.mus	-----	-----	-----	-----	-----	-----
gal9-1	-----	-----	-----	-----	-----	-----
gal	-----	-----	-----	-----	-----	-----
leg7	-----	-----	-----	-----	-----	-----
gal4	-----	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----	-----
	51					100
leg2	-----	-----	-----	-----	-----	-----
leg1	-----	-----	-----	-----	-----	-----
PCTA	-----	-----	-----	-----	-----	-----
PCTA.var	-----	-----	-----	-----	-----	-----
PCTA.mus	-----	-----	-----	-----	-----	-----
gal9-1	-----	-----	-----	-----	-----	-----
gal	-----	-----	-----	-----	-----	-----
leg7	-----	-----	-----	-----	-----	-----
gal4	-----	-----	-----	-----	-----	-----M
Consensus	-----	-----	-----	-----	-----	-----
	101					150
leg2	-----	----MTGELE	VKNMDMKPGS	TLKITGSIAD	.GTDGFVINL	
leg1	-----	----ACGLV	ASNLNLPKGE	CLRVGEVAP	.DAKSFVLNL	
PCTA	MLSLNNLQNI	IYNPVIPIYVG	TIPDQLDPGT	LIVICGHV.P	SDADRFQVDL	
PCTA.var	MLSLNNLQNI	IYNPVIPIYVG	TIPDQLDPGT	LIVICGHV.P	SDADRFQVDL	
PCTA.mus	MLSLNNLQNI	IYNPIPIYVG	TITEQLKPGS	LIVIRGHV.P	KDSERFQVDF	
gal9-1	-MAFSGSQAP	YLSPAVPFSG	TIQGGQLDGL	QITVNGTVLS	SSGTRFAVNF	
gal	-MAFSGSQAP	YLSPAVPFSG	TIQGGQLDGL	QITVNGTVLS	SSGTRFAVNF	
leg7	-----	---SNVPHKS	SLPEGIRPGT	VLRIRG.LVP	PNASRFHVN	
gal4	AYVPAPGYQP	TYNPTLPYYQ	PIPGGLNVGM	SVYIQG.VAS	EHMKRFFVNF	
Consensus	-----	---P--P---	-IP-GL-PG-	---I-G-V-P	--A-RF-VNL	

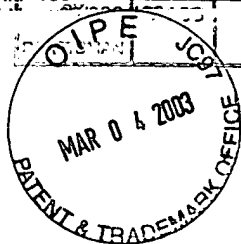
FIG. 7A



9/11

	151		200
leg2	GQGTD..... KLNLFHFNPRF	S....ESTIV	CNSLDGSMWG QEQRDHLCPF
leg1	GKDSN..... NLCLHFHFNPRF	NAHGDANTIV	CNSKDGGAWG TEQREAVFPF
PCTA	QNGSSVKPRA DVAFHFHFNPRF	K.RAGC. IV	CNTLINEKWG REEITYDTPF
PCTA.var	QNGSSVKPRA DVAFHFHFNPRF	K.RAGC. IV	CNTLINEKWG REEITYDTPF
PCTA.mus	QLGNSLKPRA DVAFHFHFNPRF	K.RSSC. IV	CNTLTQEKWG WEEITYDMPF
gal9-1	QTGFS...GN DIAFHFNPRF	E.DGGY. VV	CNTRQNGSWG PEERKTHMPF
gal	QTGFS...GN DIAFHFNPRF	E.DGGY. VV	CNTRQNGSWG PEERRTHMPF
leg7	LCGEE..QGS DAALHFHFNPRF	D..TSE. VV	FNSKEQGSWG REERGPVVPF
gal4	VVGQD..PGS DVAFHFHFNPRF	D.GWDK..VV	FNTLQGGKWG SEERKRSMFP
Consensus	--G-----G- D-AFHFNPRF	-----VV	CNT---G-WG -EER----PF
	201		250
leg2	SPGSEVKFTV TFESDKFKVK	LPDGHELTFF	NRLG.HSHLS YLSVRGGFNM
leg1	QPGSVAEVC I TFDQANLTVK	LPDGYEFKFP	NRLN.LEAIN YMAADGDFKI
PCTA	KREKSFEIVI MVLKDKFQVA	VNGKHTLLYG	HRI.GPEKID TLGIYGVNI
PCTA.var	KREKSFEIVI MVLKDKFQVA	VNGKHTLLYG	HRI.GPEKID TLGIYGVNI
PCTA.mus	RREKSFEIVF MVLKNKFQVA	VNGRHVLLYA	HRI.SPEQID TVGIYGVNI
gal9-1	QKGMPFDLCF LVQSSDFKVM	VNGILFVQYF	HRV.PFHRVD TISVNGSVQL
gal	QKGMPFDLCF LVQSSDFKVM	VNGILFVQYF	HRV.PFHRVD TIFVNGSVQL
leg7	QRGQPFEVLI IASDDGFKAV	VGDAQYHHFR	HRL.PLARVR LVEVGGDVQL
gal4	KKGAAFELVF IVLAEHYKVV	VNGNPFYEYG	HRL.PLQMVT HLQVDGDLQL
Consensus	--G--FE--- -V--D-FKV-	VNG-----Y-	HRL-PL--V- ---V-GDVQL
	251		300
leg2	SSFKLKE----	-----	-----
leg1	KCVAFD----	-----	-----
PCTA	HSIGFSFSSD LQSTQASSLE	LTEISRENV	KSGTPQL... ..
PCTA.var	HSIGFSFSSD LQSTQASSLE	LTEISRENV	KSGTPQLPSN RGGDISKIAP
PCTA.mus	HSIGFRFSSD LQSMETSALG	LTQINRENIQ	KPGKLQL... ..
gal9-1	SYISFQNPRT VPVQPAFSTV	PFSQPVCPPP	RPRGRRQKPP GVWPANPAPI
gal	SYISFQ....PP GVWPANPAPI
leg7	DSVRIF-----	-----	-----
gal4	QSINFI....GGQP .LRPQGPPMM
Consensus	-SI-F-----	-----	-----

FIG. 7B



10/11

	301				350
leg2	-----	-----	-----	-----	-----
leg1	-----	-----	-----	-----	-----
PCTAS	..LPFAARLN	TPMGPGRTVV
PCTA.var	RTVYTKSKDS	TVNHTLTCTK	IPPMNYVSKS	..LPFAARLN	TPMGPGRTVV
PCTA.musS	..LPFEARLN	ASMGPGRTVV
gal9-1	TQTVIHTVQS	APGQMFSTPA	IPPMYHPHA	YPMPFITTIL	GGLYPSKSIL
gal	TQTVIHTVQS	APGQMFSTPA	IPPMYHPHA	YPMPFITTIL	GGLYPSKSIL
leg7	-----	-----	-----	-----	-----
gal4	PPYPGPGHCH	QQLNSLPTME	GPPTFNP...	.PVPYFGRLQ	GGLTARRTII
Consensus	-----	-----	-----	---P-----	-----
	351				400
leg2	-----	-----	-----	-----	-----
leg1	-----	-----	-----	-----	-----
PCTA	VKGEVNANAK	SFNVDLLAGK	SKDIALHLNP	RLNIKAFVRN	SFLQESWGEE
PCTA.var	VKGEVNANAK	SFNVDLLAGK	SKDIALHLNP	RLNIKAFVRN	SFLQESWGEE
PCTA.mus	IKGEVNTNAR	SFNVDLVAGK	TRDIALHLNP	RLNVKAFVRN	SFLQDAWGEE
gal9-1	LSGTVLPSAQ	RFHIN..LCS	GNHIAFHLNP	RFDENAVVRN	TQIDNSWGSE
gal	LSGTVLPSAQ	RFHIN..LCS	GNHIAFHLNL	RFDENAVVRN	TQIDNSWGSE
leg7	-----	-----	-----	-----	-----
gal4	IKGYVPPTGK	SFAINFKVGS	SGDIALHINP	RMGNGTVVRN	SLLN SG WGSE
Consensus	--G-V-----	-F-----	---IA-H-N-	R-----VRN	-----WG-E
	401				450
leg2	-----	-----	-----	-----	-----
leg1	-----	-----	-----	-----	-----
PCTA	ERNIT.SFPF	SPGMYFEMII	YCDVREFKVA	VNGVHSLEYK	HRFKELSSID
PCTA.var	ERNIT.SFPF	SPGMYFEMII	YCDVREFKVA	VNGVHSLEYK	HRFKELSSID
PCTA.mus	ERNIT.CFPF	SSGMYFEMII	YCDVREFKVA	INGVHSLEYK	HRFKDLSSID
gal9-1	ERSLPRKMPF	VRGQSFSVWI	LCEAHCLKVA	VDGQHLFEYY	HRLRNLPTIN
gal	ERSLPRKMPF	VRGQSFSVWI	LCGAHCLKVA	VDGQHLFEYY	HRLRNLPTIN
leg7	-----	-----	-----	-----	-----
gal4	EKKITHN ..PF	GPGQFFDL SI	RCGLDRFKVY	ANGQHLFDFA	HRLSAFORVD
Consensus	E-----PF	--G--F---I	-C-----KV-	--G-H-----	HR-----

FIG. 7C



	451	466
leg2	~~~~~	~~~~~
leg1	~~~~~	~~~~~
PCTA	TLEINGDIHL	LEVRSW
PCTA.var	TLEINGDIHL	LEVRSW
PCTA.mus	TLSDVGDIRL	LDVRSW
gal9-1	RLEVGGDIQL	THVQT~
gal	RLEVGGDIQL	THVQT~
leg7	~~~~~	~~~~~
gal4	TLEIQGDVTL	SYVQI~
Consensus	-L---GD--L	--V---

■ Galactoside binding site

FIG. 7D